

1 CTGCTTCCACCAAGACAACCACTGAGAGCCGAGCCGAGCACTGGAAACATG
-----+-----+-----+-----+-----+-----+
60 GACGAAGGCGTGTCTTCTGCTGACCTCTCGGCTCGGCTCGTGCACCCCTTGTAC
M

61 AAGAGCGTCTTGTCTGACCAACGCTCCTCGTGCCTGCACACCTGGTGGCCCTGAGC
-----+-----+-----+-----+-----+-----+
120 TTCTCGCAGAACGACGACTGGTGCAGAGCAGCAGCAGTGTGACCAACGGCGGACCTCG
K S V L L L T T L L V P A H L Y A A W S

121 AATTAATTATGCGGTGACTGCCCTCAACACTGTGACAGCAGTGAAGCAAAAGCAGCCCG
-----+-----+-----+-----+-----+-----+
180 TTATTAAATACGCCACCTGACGGAGTTGTGACACTGTGCTCACTCAGCTTTCGTGGGC
N N Y A V D C P Q H C D S S E C K S S P

181 CGCTGCAAGAGGACAGTGTCTGACGACTGTGCTGCTGCCGAGTGTGCGCTGCAGGGCGG
-----+-----+-----+-----+-----+-----+
240 GCGACGTTCTCTGTTCACGAGCTGTGACACGAGCAGCGGCTCACACGCGACGTTCCGCC
R C K R T V L D D C G C C R V C A A G R

MATCH WITH FIG. 1B
FIG. 1A

MATCH WITH FIG. 1A

241

GGAGAACTTGTACCGCACAGTCTCAGGCATGATGGCATGAAGTGTGCCCCGGGCTG
 -----+-----+-----+-----+-----+-----+-----+
 CCTCTTTGAACGATGGCGGTGTACAGACTCCGTAACCTTACCCTTACTTACACACCGGCCCCGAC
 G E T C Y R T V S G M D G M K C G P G L

300

301

AGGTGTCAGCCCTTCTAATGGGAGGATCCTTTTGGTGAAGAGTTTGTATCTGCAAGAC
 -----+-----+-----+-----+-----+-----+-----+
 TCCACAGTCGGAAGATTACCCCTCCTAGGAAACCACCTTCTCAAAACCATAGACGTTTCTG
 R C Q P S N G E D P F G E E F G I C K D

360

361

TGTCCTTACGGCACCTTGGGATGATTGCAGAGACCTGCAACTGCACTGCCAGTCAGGCATC
 -----+-----+-----+-----+-----+-----+-----+
 ACAGGATGCGGTGAAGCCCTTACCTAACGTCTCTGTGACGTTGACGGTCACTCCGTAAG
 C P Y G T F G M D C R E T C N C Q S G I

420

421

TGTGACAGGGGGACGGGAAATGCCCTGAATTCCTTCCATATTCAGTAACCAAG
 -----+-----+-----+-----+-----+-----+-----+
 ACACTGTCCCCCTGCCCTTTTACGACTTTAAGGGGAAGAAGTTATTAAGTCAATTGGTTTC
 C D R G T G K C L K F P F F Q Y S V T K

480

MATCH WITH FIG. 1C

FIG.1B

MATCH WITH FIG. 1B

481 TCTTCCACAGATTGTTTCTCTCACCGGACATGACATGGCATCTGGAGATGCCAATATT
-----+-----+-----+-----+-----+-----+-----+
540 AGAAGGTTGTCTAAACAAGAGAGTGCCCTGTAAGTACCGTAGACCTTACCGTTATAA

S S N R F V S L T E H D M A S G D G N I

541 GTGAGAGAAGAGTTGTGAAGAAGAAATGCTGCCGGCTCTCCCGTAATGAGGAATGCTTA
-----+-----+-----+-----+-----+-----+-----+
600 CACTCTCTTCTTCAACACTTTCTCTTACGACGGCCAGAGGGCATTAATCTCTTACCAAT

V R E E V V K E N A A G S P V M R K W L

601 AATCCACGCTGATCCCGCTGTGATTTCTGAGAGAAGGCTCTATTTTCGTGAYTGTTCAA
-----+-----+-----+-----+-----+-----+-----+
660 TTAGTGCGACTAGGGCCGACACTAAAGACTCTCTTCCGAGATAAAGCACTRACAAGTT

N P R *

661 CACACAGCCAAACATTTTAGGAATTTCTAGATTTATGACATAAGACATGTAATTTTGAA
-----+-----+-----+-----+-----+-----+-----+
720 GTGTGTGGGTTGTAAAATCCTTGAAAGATCTAATATCGTATTCCTGTACATTAAAAACTT

721 GACCAAAATGTGATGCATGTGTGATCCAGAAAACAAGTAAGATTAATCAATCCATAA
-----+-----+-----+-----+-----+-----+-----+
780 CTGGTTTACACTACGTACCAACCTAGGTCCTTTTGTGTTTTCATCCCTATGAATGTTAGGTATT

MATCH WITH FIG. 1D

FIG. 1C

MATCH WITH FIG. 1C

781
CATCCATATGACTGAACACTTGTATGTGTTGTTAAATATTCGAATGCATGTAGATTGT
-----+-----+-----+-----+-----+-----+-----+
840
GTAGGTATACTGACTTGTGAACATACACAACAATTATTAAGCTTACGTACATCTAAACA

841
TAAATGTGTGTATAGTAACACTGAAGAACTAAAAAATGCAATTAGGTAATCTTACATG
-----+-----+-----+-----+-----+-----+-----+
900
ATTTACACACATATCATTTGTGACTTCTTGATTTTACGTTAAATCCATTAGAATGTAC

901
GAGACAGCTCAACCAAGAGGGAGCTAGGCCAAAGCTGAAGACCGCAGTGAGTCAAATTAG
-----+-----+-----+-----+-----+-----+-----+
960
CTCTGTCCAGTTGGTTTCTCCCTCGATCCGTTTCGACTTCTGGCGTCACCTCAGTTTAAATC

961
TTCTTTGACTTTGATGTACATTAATGTTGGGATATGGAATGAAGACTTAAAGAGCAGGAGA
-----+-----+-----+-----+-----+-----+-----+
1020
AAGAAGCTGAAGCTACATGTAAATTACAACCCCTATACCTTACTTCTGAATTCTCGTCTCT

1021
AGATGGGGAGGGGGTGGAGTGGGAATAAATATTTAGCCCTTCCTTGTAGGTAGCTT
-----+-----+-----+-----+-----+-----+-----+
1080
TTCTACCCCTCCCCCACCCTCAACCCTTATTTTATTAATAATCGGGAAGGAACCATCCATCGAA

MATCH WITH FIG. 1E
FIG. 1D

MATCH WITH FIG. 1D

CTCTAGAA TTTAA TTRTGT TTTTTT TTTTGGCT TTGGGAAA GTCAAAAT AAA
-----+-----+-----+-----+-----+
1081 1140

GAGATCTTAAATTAAYACGAAAAAAAAAACCGAAACCTTTTCAGTTTATTTT

1141
ACAACCGAAACCCCTGAAGGAAGTAGATGTTGAAGCTTATGGAATTTGAGTAACA
-----+-----+-----+-----+-----+-----+-----+
TGTTGCTCTTTTGGGACTTCCTTCATTCTACAAACTTCGAATACCTTTAAACTCATTTGT
1200

AACAGCTTTGANCCTGAGAGCAATTYCAAAGGCTGCTGATGTAGCCCCGGGTTNCCCTNT
 -----+-----+-----+-----+-----+-----+-----+
 1201
 TTGTCCGAACCTNGACTCTCGTTAARGTTTTTCCGACGACTTACATCGGGGCCCAANGGANA
 -----+-----+-----+-----+-----+-----+-----+

NTCTNAGGAC 1271
-----+-
NAGANTTCCTG 1261

FIG. 1E

	1		50
cel10_chick	...	MGsAGAR P.ALAALLC LARLALGSPC PAV...	CQC ... PAA.APQ
cyr6_mouse	...	MSSSTER TLAVAVTLAH LTRLAL.STC PAA...	CHC ... PLE.APK
ctgf_human	...	MTAASMGPV RVAFVLLAL CSRPVGVQNC SGP...	CRC ... PDEPAR
fisp-12	...	MLASVAGPI SLAL.VLLAL CTRTATGQDC SAQ...	CQC ... AAEAPH
nov_chick	...	METGGGQGL PLLLLLLL RPCEVSGREA ACPRPCGRC	... PAEP.PR
ibp_3human	...	MQRARPTLWA AALTLLVLLR GPPVARAGAS SGGLGPVVR	C EPCVARALAR
ccn-4	...	MK SVLLLTTLV PAHLVAAWSN MYAVDCPQHC	DSSECKSSPR

	51		100
cel10_chick	...	DGCGCC KVC AKQ LNE D C...	SRTQ P CDHTKGLECN
cyr6_mouse	...	DGCGCC KVC AKQ LNE D C...	SKTQ P CDHTKGLECN
ctgf_human	...	DGCGCC RVC AKQ LGE L C...	TERDP CDPHKGLFCD
ccn-4

	401		411
cel10_chick	...	RLVNDIHKFR D	
cyr6_mouse	...	SLFNDIHKFR D	
ctgf_human	...	YYRKMYGDMA	
fisp-12	...	YYRKMYGDMA	
nov_chick	...	DPMSSSEAKI	
ibp3_human	
ccn-4	

FIG. 2